

#### HEAVY CONSTANT CHAINS CH<sub>3</sub> REGIONS

EU INDEX	GU INDEX	INVARIANT RESIDUES	1 HUMAN IGM	2 HUMAN IGM	3 GAL	4 OU	5 BOT	6 X17115	7 GLI	8 HUMAN IGM	9 MAH	10 NIG	11 ERI	12 HUMAN IGM	13 HUMAN IGM	14 HUMAN IGM	15 OMM	16 HER	17 FRO	18 JCN	19 WIS
361	341	---	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ALA	ALA	ALA	ALA	ALA	ALA	GLY	GLY	GLY	GLY	GLY	
362	340	---	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	
363	342	341	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ALA	ALA	ALA	ALA	ALA	ALA	GLN	GLN	GLN	GLN	GLN	
364	343	342	THR	THR	THR	THR	THR	THR	THR	PRO	PRO	PRO	PRO	PRO	PRO	GLN	GLN	GLN	GLN	GLN	
365	344	343	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
366	345	344	ALA	ALA	ALA	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY		
367	346	345	ILE	ILE	ILE	ILE	ILE	ILE	ILE	LYS	LYS	LYS	LYS	LYS	GLY	GLY	GLY	GLY	GLY		
367A	346	345	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
367B	347	346	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ALA	ALA	ALA	ALA	ALA	ALA	GLN	GLN	GLN	GLN	GLN	
368	347	346	ARG	ARG	ARG	ARG	ARG	ARG	ARG	LEU	LEU	LEU	LEU	LEU	LEU	GLN	GLN	GLN	GLN	GLN	
369	348	347	VAL	VAL	VAL	VAL	VAL	VAL	VAL	SER	SER	SER	SER	SER	SER	VAL	VAL	VAL	VAL	VAL	
370	349	348	PHE	PHE	PHE	PHE	PHE	PHE	PHE	LEU	LEU	LEU	LEU	LEU	LEU	TYR	TYR	TYR	TYR	TYR	
371	349	349	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ASN	ASN	ASN	ASN	ASN	ASN	THR	THR	THR	THR	THR	
372	350	349	ILE	ILE	ILE	ILE	ILE	ILE	ILE	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
373	351	350	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ALA	ALA	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	PRO	
374	352	351	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ALA	ALA	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	PRO	
375	353	352	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
376	354	353	PHE	PHE	PHE	PHE	PHE	PHE	PHE	ASP	ASP	ASP	ASP	ASP	ASP	ARG	ARG	ARG	ARG	ARG	
377	355	354	ALA	ALA	ALA	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	PRO	PRO	GLY	GLY	GLY	GLY	GLY	
378	356	355	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
379	356	355	SER	SER	SER	SER	SER	SER	SER	---	---	---	---	---	---	---	---	---	---	---	
380	357	356	ILE	ILE	ILE	ILE	ILE	ILE	ILE	PRO	PRO	PRO	PRO	PRO	PRO	MET	MET	MET	MET	MET	
381	358	357	PHE	PHE	PHE	PHE	PHE	PHE	PHE	GLU	GLU	GLU	GLU	GLU	GLU	THR	THR	THR	THR	THR	
382	359	358	LEU	LEU	LEU	LEU	LEU	LEU	LEU	TRP	TRP	TRP	TRP	TRP	TRP	VAL	VAL	VAL	VAL	VAL	
383	360	359	THR	THR	THR	THR	THR	THR	THR	ALA	ALA	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	
384	361	360	LYS	LYS	LYS	LYS	LYS	LYS	LYS	ALA	ALA	ALA	ALA	ALA	ALA	ASN	ASN	ASN	ASN	ASN	
385	362	361	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	GLN	GLN	GLN	GLN	GLN	
386	363	362	THR	THR	THR	THR	THR	THR	THR	TRP	TRP	TRP	TRP	TRP	TRP	VAL	VAL	VAL	VAL	VAL	
387	364	363	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LEU	LEU	LEU	LEU	LEU	LEU	SER	SER	SER	SER	SER	
388	365	364	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
389	366	365	THR	THR	THR	THR	THR	THR	THR	LEU	LEU	LEU	LEU	LEU	LEU	THR	THR	THR	THR	THR	
390	367	366	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	
391	368	367	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLU	GLU	GLU	GLU	GLU	GLU	LEU	LEU	LEU	LEU	LEU	
392	369	368	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
393	370	369	THR	THR	THR	THR	THR	THR	THR	SER	SER	SER	SER	SER	SER	LYS	LYS	LYS	LYS	LYS	
394	371	370	ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
395	372	371	LEU	LEU	LEU	LEU	LEU	LEU	LEU	PHE	PHE	PHE	PHE	PHE	PHE	GLY	GLY	GLY	GLY	GLY	
396	373	372	THR	THR	THR	THR	THR	THR	THR	SER	SER	SER	SER	SER	SER	PHE	PHE	PHE	PHE	PHE	
397	374	373	THR	THR	THR	THR	THR	THR	THR	PRO	PRO	PRO	PRO	PRO	PRO	TYR	TYR	TYR	TYR	TYR	
398	375	374	TYR	TYR	TYR	TYR	TYR	TYR	TYR	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
399	376	375	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASN	ASN	ASN	ASN	ASN	ASN	ASP	ASP	ASP	ASP	ASP	
400	377	376	TRP	TRP	TRP	TRP	TRP	TRP	TRP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
401	378	377	SER	SER	SER	SER	SER	SER	SER	---	---	---	---	---	---	---	---	---	---	---	
402	379	378	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	ALA	ALA	ALA	ALA	ALA	
403	379	378	THR	THR	THR	THR	THR	THR	THR	LEU	LEU	LEU	LEU	LEU	LEU	VAL	VAL	VAL	VAL	VAL	
404	380	379	ILE	ILE	ILE	ILE	ILE	ILE	ILE	---	---	---	---	---	---	---	---	---	---	---	
405	380	381	TRP	TRP	TRP	TRP	TRP	TRP	TRP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
406	381	382	SER	SER	SER	SER	SER	SER	SER	---	---	---	---	---	---	---	---	---	---	---	
407	382	383	THR	THR	THR	THR	THR	THR	THR	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
408	383	384	ARG	ARG	ARG	ARG	ARG	ARG	ARG	GLU	GLU	GLU	GLU	GLU	GLU	SER	SER	SER	SER	SER	
409	384	385	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
410	385	386	GLN	GLN	GLN	GLN	GLN	GLN	GLN	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
411	386	386	ASN	ASN	ASP	ASP	ASP	ASP	ASP	GLN	GLN	GLN	GLN	GLN	GLN	SER	SER	SER	SER	SER	
412	387	386	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
413	386	387	GLY	GLY	GLY	GLY	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLN	GLN	GLN	
414	387	387	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
415	388	389	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLN	GLN	GLN	GLN	GLN	
416	389	390	VAL	VAL	VAL	VAL	VAL	VAL	VAL	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
417	390	391	LYS	LYS	LYS	LYS	LYS	LYS	LYS	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
418	391	392	THR	THR	THR	THR	THR	THR	THR	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
419	392	393	HIS	HIS	HIS	HIS	HIS	HIS	HIS	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
420	393	394	THR	THR	THR	THR	THR	THR	THR	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
421	394	394	ASP	ASP	ASP	ASP	ASP	ASP	ASP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
422	395	395	SER	SER	SER	SER	SER	SER	SER	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
423	396	395	THR	THR	THR	THR	THR	THR	THR	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
424	397	396	ASP	ASP	ASP	ASP	ASP	ASP	ASP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
425	398	397	GLU	GLU	GLU	GLU	GLU	GLU	GLU	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
426	399	399	ALA	ALA	ALA	ALA	ALA	ALA	ALA	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
427	400	401	ILE	ILE	ILE	ILE	ILE	ILE	ILE	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
428	401	402	CYS	CYS	CYS	CYS	CYS	CYS	CYS	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
429	402	403	VAL	VAL	VAL	VAL	VAL	VAL	VAL	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
430	403	404	HIS	HIS	HIS	HIS	HIS	HIS	HIS	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		
431	404	405	THR	THR	THR	THR	THR	THR	THR	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
432	405	406	ASP	ASP	ASP	ASP	ASP	ASP	ASP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
433	406	407	GLU	GLU	GLU	GLU	GLU	GLU	GLU	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
434	407	408	ALA	ALA	ALA	ALA	ALA	ALA	ALA	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
435	408	409	VAL	VAL	VAL	VAL	VAL	VAL	VAL	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
436	409	410	ASP	ASP	ASP	ASP	ASP	ASP	ASP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
437	410	411	LEU	LEU	LEU	LEU	LEU	LEU	LEU	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
438	411	412	LEU	LEU	LEU	LEU	LEU	LEU	LEU	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
439	412	413	PRO	PRO	PRO	PRO	PRO	PRO	PRO	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
440	413	414	LYS	LYS	LYS	LYS	LYS	LYS	LYS	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
441	414	415	GLN	GLN	GLN	GLN	GLN	GLN	GLN	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
442	415	416	ILE																		

—**HY CONSTANT CHAINS CH3 REGION (cont'd)**

EU	OU	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
INDEX	INDEX	SPA	ZUC	ZUC'	KUP	BRU	JIR	CHA	GOE	EU	NIE	CRA	VAU	LEB	EST	YOK	SAC	HUMAN	KOL	MCG	LEC	DOB	BUR	TRO	CAP

**HEAVY CONSTANT CHAINS CH3 REGION (cont'd)**

## HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU INDEX	OU INDEX	63 HUMAN IGA2 "CL	64 HUMAN IGA2 "CL	65 HUMAN IGA2 "CL	66 IGM "CL	67 IGM "CL	68 IGM-b "CL	69 MUTANT 102 "CL	70 MOPC 104E "CL	71 MOPC 104E "CL	72 HPC76 "CL	73 G8 "CL	74 GAT50 "CL	75 IGD "CL	76 SECR "CL	77 IGC "CL	78 B1-8 "CL	79 MOUSE 1993 "CL	80 IGG3 "CL
361	341	GLY	GLY	---	SER	SER	SER	---	SER	---	---	---	---	---	---	---	---	GLY	GLY
362	340	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
363	342	ASN	ASN	PRO	PRO	PRO	PRO	PRO	PRO	PRO	---	---	---	---	---	---	---	ALA	GLY
364	343	THR	THR	THR	THR	THR	THR	THR	THR	THR	---	---	---	---	---	---	---	---	---
365	344	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	---	---	---	---	---	---	---	---	---
366	345	344	ARG	ARG	ASP	ASP	ASP	ASP	ASP	ASP	---	---	---	---	---	---	---	ALA	ALA
367	346	345	PRO	PRO	ILE	ILE	ILE	ILE	ILE	ILE	---	---	---	---	---	---	---	PRO	PRO
367A	347	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
367B	348	346	GLU	GLU	LEU	LEU	LEU	LEU	LEU	LEU	---	---	---	---	---	---	---	GLN	GLN
368	347	346	VAL	VAL	THR	THR	THR	THR	THR	THR	---	---	---	---	---	---	---	VAL	VAL
369	348	347	HIS	HIS	PHE	PHE	PHE	PHE	PHE	PHE	---	---	---	---	---	---	---	TYR	TYR
370	349	348	LEU	LEU	THR	THR	THR	THR	THR	THR	---	---	---	---	---	---	---	THR	THR
371	350	349	LEU	LEU	ILE	ILE	ILE	ILE	ILE	ILE	---	---	---	---	---	---	---	ILE	ILE
372	351	350	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	---	---	---	---	---	---	---	PRO	PRO
373	352	351	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
374	353	352	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	---	---	---	---	---	---	---	PRO	PRO
375	354	353	PRO	PRO	SER	SER	SER	SER	SER	SER	---	---	---	---	---	---	---	LYS	LYS
376	355	354	GLU	GLU	PHE	PHE	PHE	PHE	PHE	PHE	---	---	---	---	---	---	---	ARG	GLN
377	356	355	GLU	GLU	ALA	ALA	ALA	ALA	ALA	ALA	---	---	---	---	---	---	---	GLN	GLN
378	357	356	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
379	358	357	LEU	LEU	ILE	ILE	ILE	ILE	ILE	ILE	---	---	---	---	---	---	---	---	---
380	359	358	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	---	---	---	---	---	---	---	---	---
381	360	359	ASN	ASN	SER	SER	SER	SER	SER	SER	---	---	---	---	---	---	---	---	---
382	361	360	GLU	GLU	LYS	LYS	LYS	LYS	LYS	LYS	---	---	---	---	---	---	---	---	---
383	362	361	LEU	LEU	SER	SER	SER	SER	SER	SER	---	---	---	---	---	---	---	---	---
384	363	362	VAL	VAL	ALA	ALA	ALA	ALA	ALA	ALA	---	---	---	---	---	---	---	---	---
385	364	363	THR	THR	ASN	ASN	ASN	ASN	ASN	ASN	---	---	---	---	---	---	---	---	---
386	365	364	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	---	---	---	---	---	---	---	---
387	366	365	THR	THR	THR	THR	THR	THR	THR	THR	---	---	---	---	---	---	---	---	---
388	367	366	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	---	---	---	---	---	---	---	THR	THR
389	368	367	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	---	---	---	---	---	---	CYS	CYS
390	369	368	ALA	ALA	VAL	VAL	VAL	VAL	VAL	VAL	---	---	---	---	---	---	---	MET	MET
391	370	369	ARG	ARG	SER	SER	SER	SER	SER	SER	---	---	---	---	---	---	---	ALA	ALA
392	371	370	GLY	GLY	ASN	ASN	ASN	ASN	ASN	ASN	---	---	---	---	---	---	---	GLU	GLU
393	372	371	PHE	PHE	ASN	ASN	ASN	ASN	ASN	ASN	---	---	---	---	---	---	---	ASP	ASP
394	373	372	SER	SER	ALA	ALA	ALA	ALA	ALA	ALA	---	---	---	---	---	---	---	THR	THR
395	374	373	PRO	PRO	THR	THR	THR	THR	THR	THR	---	---	---	---	---	---	---	PHE	PHE
396	375	374	LYS	LYS	TYR	TYR	TYR	TYR	TYR	TYR	---	---	---	---	---	---	---	GLU	GLU
397	376	375	ASP	ASP	ILE	ILE	ILE	ILE	ILE	ILE	---	---	---	---	---	---	---	TRP	TRP
398	377	376	ASP	ASP	GLU	GLU	GLU	GLU	GLU	GLU	---	---	---	---	---	---	---	GLU	GLU
399	378	377	VAL	VAL	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
400	379	378	LEU	LEU	THR	THR	THR	THR	THR	THR	---	---	---	---	---	---	---	---	---
401	380	379	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
402	381	380	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
403	382	381	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
404	383	382	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
405	384	383	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
406	385	384	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
407	386	385	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
408	387	386	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
409	388	387	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
410	389	388	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
411	390	389	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
412	391	390	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
413	392	391	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
414	393	392	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
415	394	393	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
416	395	394	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
417	396	395	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
418	397	396	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
419	398	397	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
420	399	398	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
421	400	399	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
422	401	400	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
423	402	401	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
424	403	402	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
425	404	403	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
426	405	404	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
427	406	405	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
428	407	406	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
429	408	407	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
430	409	408	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
431	410	409	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
432	411	410	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
433	412	411	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
434	413	412	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
435	414	413	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
436	415	414	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
437	416	415	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
438	417	416	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
439	418	417	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
440	419	418	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
441	420	419	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
442	421	420	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
443	422	421	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
444	423	422	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
445	424	423	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
446	425	424	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
447	426	425	---																

## HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU INDEX	OU INDEX	82 MEMB 'CL	83 MOPC 'CL	84 IGG1 'CL	85 IGG2 'CL	86 IGG2B 'CL	87 (B) 'CL	88 IGG2B 'CL	89 IGG2B 'CL	90 MPC 'CL	91 10.1 'CL	92 IGG2A 'CL	93 17/9 'CL	94 IGG2A 'CL	95 IGG2A 'CL	96 MEMB 'CL	97 MOPC 'CL	98 CBPC 'CL	99 IGA 'CL	100 IGG 'CL	
361	341		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		
362	340		---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
363	341		LYS	SER	LEU	LEU	LEU	LEU	LEU	SER		PRO	POO	SER	PRO ASN	VAL	VAL	VAL	VAL		
364	342		PRO	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		
365	343		ARG		ARG	ARG	ARG	ARG	ARG	ARG		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		
366	345	344	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		
367	346	345	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		
367A		---	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
367B		---	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
368	347	346	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		
369	348	347	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		
370	349	348	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		
371	350	349	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR		
372	351	350	ILE	LEU	LEU	LEU	LEU	LEU	LEU	LEU		ILE	LEU	LEU	LEU	LEU	LEU	LEU	LEU		
373	352	351	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		
374	353	352	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		
375	354	353	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		
376	355	354	LYS	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
377	356	355	GLU	ALA	ALA	ALA	ALA	ALA	ALA	ALA		GLU	ALA	ALA	ALA	GLX	ALA SER	GLU	GLU		
378	357	355	GLN	GLU	GLU	GLU	GLU	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLX	ALA GLU	GLU	GLU		
379		356	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
380		357	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
381	358	358	MET	LEU	LEU	LEU	LEU	LEU	LEU	MET		MET	MET	MET	MET	ALA	ALA	ALA	ALA		
382	359	359	ALA	SER	SER	SER	SER	SER	SER	THR		THR	THR	THR	THR	THR	THR	THR	THR		
383	360	360	LYS	ARG	ARG	ARG	ARG	ARG	ARG	LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		
384	361	361	ASP	LYS	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		
385	362	362	LYS	ASP	ASP	ASP	ASP	ASP	ASP	ASP		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		
386	363	363	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	PHE	PHE	PHE	PHE	LEU	LEU	LEU		
387	364	364	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER		
388	365	365	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		
389	366	366	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR		
390	367	367	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		
391	368	368	MET	LEU	LEU	LEU	LEU	LEU	LEU	MET		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		
392	369	369	ILE	VAL	VAL	VAL	VAL	VAL	VAL	ILE		VAL	ILE	ILE	ILE	ILE	ILE	ILE	ILE		
393	370	370	THR	VAL	VAL	VAL	VAL	VAL	VAL	THR		THR	THR	THR	THR	THR	THR	THR	THR		
394	371	371	ASP	ILE	ILE	ILE	ILE	ILE	ILE	ASP		ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY		
395	372	372	PHE	PRO	PRO	PRO	PRO	PRO	PRO	PHE		PHE	PRO	PRO	PRO	PRO	PRO	PRO	PRO		
396	373	373	PHE	ASN	ASN	ASN	ASN	ASN	ASN	PHE		PHE	ASN	ASN	ASN	ASN	ASN	ASN	ASN		
397	374	374	PRO	GLU	GLU	GLY	GLY	GLY	GLU	PRO		PRO	GLU	GLU	GLU	GLU	GLU	GLU	GLU		
398	375	375	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
399	376	376	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		
400	377	377	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		
401	378	377	THR	TYR	SER	SER	SER	SER	SER	THR		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		
402	379	378	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		
403		379	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
404		380	380	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
405	380	381	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		GLU	ASP	ASP	ASP	ASP	GLU	ASP	ASP		
406	381	382	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		
407	382	383	GLN	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR		
408	383	384	SER	ASN	SER	SER	SER	SER	SER	SER		ASN	SER	SER	SER	SER	SER	SER	SER		
409		376	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
410	384	385	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		
411	385	386	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		
412		386	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
413		387	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
414	386	387	GLN	LYS	HIS	HIS	HIS	HIS	HIS	HIS		LYS	ARG	ARG	ARG	ARG	GLU	GLU	GLU	GLU	
415	387	388	ALA	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	
416	388	389	PRO	GLU	GLU	GLU	GLU	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	
417	389	390	GLU	LEU	GLU	GLU	GLU	GLU	GLU	GLU		LEU	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	
418	390	391	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	
419	391	392	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	
420	392	393	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
421	393	394	ASN	ASN	ASP	ASP	ASP	ASP	ASP	ASP		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	
422	394	395	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	
423	395	396	GLN	GLU	ALA	ALA	ALA	ALA	ALA	ALA		GLU	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	
424	396	397	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
425	397	398	ILE	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
426	398	399	MET	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
427	399	400	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
428	400	401	THR	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	
429		401	402	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
430		401	402	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
431		402	403	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
432		403	404	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	
433		404	405	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	
434		405	406	PHE	PHE	PHE	PHE	PHE	PHE	PHE		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
435		406	407	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
436		407	408	TYR</																	

**HEAVY CONSTANT CHAIRS CH3 REGION (cont'd)**

## HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU INDEX	OU INDEX	123 IGG	124 BI-12	125 PGAMMA	126 RAB	127 RAB	128 P2A2	39-1A, *CL	129 PA19	130 CT-12	131 PIKA	132 HA-3	133 HA-11	134 HA-1	135 HA-5	136 HA-LT	137 SYRIAN	138 GP	139 GP	140 GP	141 MOC	
361	341			GLY	GLY	GLY	GLY	---			GLY						---	GLY	GLY	GLY	---	
362	340			---					VAL		---						SER	---	---	ASP		
363	342	341		GLN	GLU	GLN	GLN	GLN	VAL		GLU						PRO	PRO	PRO	ALA	GLN	
364	343	342		PRO	PRO	PRO	PRO	PRO	THR		ALA						SER	PRO	PRO	PRO	PRO	
365	344	343		LEU	LEU	LEU	LEU	LEU	---	LEU							THR	ARG	ARG	ARG	VAL	
366	345	344		GLU	GLU	GLU	GLU	GLU	PRO	PRO	GLU						ASP	ILE	ILE	MET	GLY	
367	346	345		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO						ILE	PRO	PRO	PRO	ILE	
368	347	346		---	---	---	---	---	---	---	---						---	---	---	---	---	
369	348	347		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		ALA	VAL	VAL	VAL	ILE	
370	349	348		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		PHE	TYR	TYR	TYR	PHE	
371	350	349		THR	THR	THR	THR	THR	LEU	THR	VAL	VAL	THR	THR	THR		PRO	ILE	ILE	THR	THR	
372	351	350		MET	MET	MET	MET	MET	LEU	LEU	LEU	LEU	LEU	LEU	LEU		ASP	ILE	ILE	ILE	ILE	
373	352	351		GLY	GLY	GLY	GLY	GLY	PRO	GLY	ALA						ILE	LEU	LEU	LEU	ILE	
374	353	352		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	
375	354	353		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		SER	PRO	PRO	PRO	PRO	
376	355	354		ARG	ARG	ARG	ARG	ARG	---	---	---	---	---	---	---		ASP	ARG	ASP	ASP	ASP	
377	356	355		GLU	GLU	GLU	GLU	GLU	SER								PHE	ASP	ASP	ASP	PHE	
378	357	355		GLU	GLN	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		VAL	GLX	GLU	GLU	ALA	
379	358	357		---	---	---	---	---	---	---	---	---	---	---	---		GLY	---	---	---	SER	
380	358	358		LEU	LEU	LEU	LEU	LEU	ALA								ILE	---	---	---	ILE	
381	359	359		SER	SER	SER	SER	SER	LEU								PHE	LEU	LEU	LEU	ILE	
382	360	360		SER	SER	SER	SER	SER	ASN								LEU	SER	SER	SER	ASN	
383	360	360		---	---	---	---	---	---	---	---	---	---	---	---		ASN	LYS	LYS	LYS	THR	
384	361	361		ARG	ARG	ARG	ARG	ARG	GLU								LYS	LYS	LYS	SER	LYS	
385	362	362		SER	SER	SER	SER	SER	GLN								SER	LYS	LYS	SER	LYS	
386	363	363		VAL	VAL	VAL	VAL	VAL	VAL								ALA	VAL	VAL	VAL	ALA	
387	364	364		SER	SER	SER	SER	SER	THR								THR	SER	SER	SER	LYS	
388	365	365		LEU	LEU	LEU	LEU	LEU	LEU								LEU	LEU	LEU	VAL	LEU	
389	366	366		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	SER	
390	367	367		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS	CYS	CYS	
391	368	368		MET	MET	MET	MET	MET	LEU								LEU	MET	MET	MET	LEU	
392	369	369		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		VAL	ILE	ILE	ILE	VAL	
393	370	370		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN		THR	THR	THR	THR	THR	
394	371	371		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		ASN	GLY	GLY	GLY	ASN	ASP
395	372	372		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		ILE	PHE	PHE	PHE	PHE	ASP
396	373	373		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		ALA	TYR	TYR	TYR	TYR	ALA
397	374	374		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		THR	PRO	PRO	PRO	PRO	THR
398	375	375		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		TYR	ALA	ALA	ALA	ALA	TYR
399	376	376		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP
400	377	377		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		THR	ASN	ASN	HIS	SER	
401	378	377		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		LEU	VAL	VAL	VAL	VAL	ILE
402	379	378		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		ASN	---	---	---	---	THR
403	379	379		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	
404	380	380		---	---	---	---	---	---	---	---	---	---	---	---		ILE	SER	---	---	---	
405	380	381		GLU	GLY	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		TRP	TRP	TRP	TRP	TRP	TRP
406	381	382		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		SER	ASP	ASP	ASP	ASP	ASP
407	382	383		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		SER	ASP	ASP	ASP	ASP	ASP
408	383	384		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		SER	ASP	ASP	ASP	ASP	ASP
409	384	385		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	
410	385	386		ASN	ASP	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN		ARG	SER	SER	ASN	GLU	
411	386	386		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		---	---	---	---	---	
412	386	386		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	
413	387	387		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	
414	386	387		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		GLY	---	---	---	---	
415	387	388		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		GLU	SER	SER	GLY	---	
416	388	389		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		PRO	ASP	ASP	GLU	ALA	
417	389	390		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		LEU	---	---	LYS	LEU	
418	390	391		ASN	ASP	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN		GLU	---	---	---	---	
419	391	392		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	---	---	---	---	
420	392	393		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		LYS	---	---	---	---	
421	393	394		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	ASN	ASN	ASN	THR	
422	394	395		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	
423	395	396		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		---	---	---	---	---	
424	396	397		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		LEU	PRO	PRO	PRO	PRO	
425	397	398		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		SER	PHE	PHE	PHE	PHE	
426	398	399		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		PRO	ASP	ASP	ASP	ASP	
427	399	400		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		GLU	---	---	---	---	
428	400	401		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	
429	401	402		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		PRO	SER	THR	ALA	PRO	
430	401	402		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASN	ASP	ASP	ASP	ASP	
431	402	403		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLU	GLY	GLY	GLY	
432	403	404		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	SER	THR	THR	THR	
433	404	405		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		PHE	PHE	PHE	PHE	PHE	
434	405	406		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	
435	406	407		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	
436	407	408		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		ILE	TYR	TYR	TYR	TYR	TYR
437	409	410		LYS	LYS	LYS	LYS	LYS														

## HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU INDEX	OU INDEX	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156
PSRC	PSRC	PIG	SHEEP	HORSE	BOVINE	GOAT	CHICKEN	Elops	Re2b	Re20	Xenopus	Xenopus	Xenopus	Xenopus	Xenopus	Xenopus
IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGM	VR	'CL	'CL	Xeavis	Xeavis	Xeavis	Xeavis	Xeavis	Xeavis
		8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
361	341			GLY												
362	340			---												
363	342	341		GLN												
364	343	342		ALA												
365	344	343		ARG												
366	345	344		GLU												
367	346	345		PRO												
367A				---												
367B				---												
368	347	346		GLN												
369	348	347		VAL												
370	349	348		TYR												
371	350	349		VAL												
372	351	350		LEU												
373	352	351		ALA												
374	353	352		PRO												
375	354	353		PRO												
376	355			GLN												
377	356	354		GLU												
378	357	355		GLU												
379		356		---												
380		357		---												
381	358	358		LEU												
382	359	359		SER												
383	360	360		LYS												
384	361	361		SER												
385	362	362		THR												
386	363	363		LEU												
387	364	364		SER												
388	365	365		VAL												
389	366	366		THR												
390	367	367		CYS												
391	368	368		LEU												
392	369	369		VAL												
393	370	370		THR												
394	371	371		GLY												
395	372	372		PHE												
396	373	373		TYR												
397	374	374		PRO												
398	375	375		ASP												
399	376	376		TYR												
400	377			ILE												
401	378	377		ALA												
402	379	378		VAL												
403		379		---												
404		380		---												
405	380	381		GLU												
406	381	382		TRP												
407	382	383		GLN												
408	383	384		LYS												
409				---												
410	384	385		ASN												
411	385	386		GLY												
412				GLN												
413				PRO												
414	386	387		GLU												
415	387	388		SER												
416	388	389		GLU												
417	389	390		ASP												
418	390	391		LYS												
419	391	392		TYR												
420	392	393		GLY												
421	393	394		THR												
422	394	395		THR												
423	395	396		THR												
424	396	397		SER												
425	397	398		GLU												
426	398	399		LEU												
427	399	400		ASP												
428	400	401		ALA												
429		401	402	ASP												
430		401	402	ASN												
431				---												
432				ASP												
433	402	403		GLY												
434	403	404		SER												
435	404	405		TYR												
436	405	406		PHE												
437	406	407		LEU												
438	407	408		TYR												
439	408	409		SER												
440	409	410		ARG												
441	410	411		LEU												
442	411	412		ARG												
443	412	413		VAL												
444	413	414		ASP												
445	414	415		LYS												
446	415	416		ASN												
447	416	417		SER												
448	417	418		TRP												
449	418	419		GLN												
450	419	420		---												
451	420	421		GLY												
452	421	422		ASP												
453	422	423		THR												
454	423	424		TYR												
455	424	425		ALA												
456	425	426		CYS												
457	426	427		VAL												
458	427	428		VAL												
459	428	429		MET												
460	429	430		BIS												
461	430	431		GLU												
462	431	432		ALA												
463	432	433		LEU												
464	433	434		HIS												
465	434	435		ASN												
466	435	436		HIS												
467	436	437		TYR												
468	437			THR												
469	438	438		GLN												
470	439	439		LYS												
471	440	440		SER												
472	441	441		ILE												
473	442	442		---												
474	443	443		SER												
475	444	444		PRO												
476	445	445		PRO												
477	446	446		GLY												
478				LYS												

## HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU INDEX	OU INDEX	157 Xenopus laevis	158 Xenopus laevis	159 Xenopus laevis	SEQUENCES 34(III) 'CL	# OF AMINO ACIDS	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
361	341				74	5	54(GLY)	6.9	
362	342	340			37	8	11(SER)	27.	
363	342	341			89	14	33(GLN), 32(GLN)	38., 39.	
364	343	342			90	10, 11	43(PRO)	21., 23.	
365	344	343			91	10	45(ARG)	20.	
366	345	344			92	13	24(GLU), 23(GLU)	50., 52.	
367	346	345			92	9	50(PRO)	17.	
367A					95	4	2(THR)		
367B					95	1	5(PRO)		
368	347	346			91	10	43(GLN), 40(GLN)	21., 23.	
369	348	347			93	6	65(VAL)	8.6	
370	349	348			93	10	57(TYR)	16.	
371	350	349			94	4	39(THR)	17.	
372	351	350			94	5	48(LEU)	9.8	
373	352	351			93	7	68(PRO)	9.6	
374	353	352			93	3	87(PRO)	3.2	
375	354	353			93	4	51(SER)	7.3	
376	355				93	6	24(ARG)	14.	
377	356	354			88	11, 13	32(GLU), 29(GLU)	33., 41.	
378	357	355			91	10	49(GLU), 45(GLU)	19., 23.	
379	356				36	5	14(GLU)		
380	357				88	5	28(LEU)	8.6	
381	358	358			92	7	26(MET)	25.	
382	359	359			92	10	27(LEU)	34.	
383	360	360			92	10, 11	32(LYS)	29., 32.	
384	361	361			91	10	33(LYS)	28.	
385	362	362			91	8	32(SER)	23.	
386	363	363			91	8	48(VAL)	15.	
387	364	364			84	5	41(SER)	10.	
388	365	365			92	4	61(LEU)	4.5	
389	366	366			92	6	52(GLY)	11.	
390	367	367			92	6	61(PHE)	7.5	
391	368	368			91	5	51(TYR)	33.	
392	369	369			91	6	65(LEU)	8.4	
393	370	370			92	9	66(VAL)	6.9	
394	371	371			92	9	22(THR)	38.	
395	372	372			92	5	52(GLY)	11.	
396	373	373			92	11	61(PHE)	7.5	
397	374	374			92	6	57(VAL)	8.2	
398	375	375			93	10	30(SER)	31.	
399	376	376			93	10	59(ASP), 56(ASP)	16., 17.	
400	377				66	4	45(ILS)	5.9	
401	378	377			91	10	28(VAL)	43.	
402	379	378			90	9	68(VAL)	12.	
403		379			31	5, 6	14(ASN), 13(+)	11., 14.	
404		380			31	4	14(ILS)	8.9	
405	380	382			92	10	36(GLU)	26.	
406	382	382			91	2	86(GLU)	2.1	
407	383	383			90	13	24(GLU), 23(GLU)	49., 51.	
408	383	384			81	10	34(SER)	24.	
409					16	6	8(GLN)	12.	
410	384	385			87	10	27(ASN), 26(ASN)	32., 33.	
411	385	386			19	4	34(GLY)	20., 23.	
412					19	4	10(GLN)	7.6	
413					28	6	12(GLU)		
414	386	387			86	11	21(GLU)	14.	
415	387	388			88	12	28(VAL)	45.	
416	388	388			88	12	44(THR)	38.	
417	389	390			83	9	19(GLU)	28., 31.	
418	390	391			86	10	37(ASN), 36(ASN)	23., 24.	
419	391	392			87	10	47(TYR)	19.	
420	392	392			89	11	40(LYS)	24.	
421	393	394			88	12	44(THR)	24.	
422	394	395			88	10, 11	37(THR)	24., 26.	
423	395	396			88	10	32(VAL)	27.	
424	396	397			88	11	37(VAL)	26.	
425	397	398			88	12	24(VAL)	44.	
426	398	399			87	13	33(LEU)	34.	
427	399	400			88	12	37(ASP)	29.	
428	400	401			84	11	35(SER)	26.	
430	401	402			16	3	11(SER)	4.4.	
431					85	6	42(ASP), 40(ASP)	12., 13.	
432					14	3	11(GLY)	3.8	
433	402	403			15	5	8(THR)	9.4	
434	403	404			88	9	54(GLY)	15.	
435	404	405			88	6	45(THR)	15.	
436	405	406			88	7	45(PHE)	14.	
437	406	407			88	7	41(PHE)	17.	
438	407	408			89	10	30(LEU)	21.	
439	408	409			89	10	42(TYR)	21.	
440	409	410			88	4	72(SER)	4.9	
441	410	411			88	7	38(LYS)	16.	
442	411	412			87	5	72(LEU)	6.1	
443	412	413			87	8	23(ARG)	30.	
444	413	414			89	5	76(VAL)	5.9	
445	414	415			80	10	26(ASP)	35.	
446	415	416			81	7	31(LYS)	21.	
447	416	417			80	11	33(SER)	30.	
448	417	418			91	10	36(ASP), 31(ASP)	25., 29.	
449	418	419			89	4	82(TRP)	4.3	
450	419	420			91	12	25(GLN), 24(GLN)	44., 45.	
451	420	421			91	10	1(ASP)		
452	421	422			90	8	1(LEU)		
453	422	423			91	9	28(GLN), 27(GLN)	32., 34.	
454	423	424			89	11	71(GLY)	10.	
455	424	425			89	11	25(ASP), 24(+)	33., 34.	
456	425	426			91	11	25(THR)	39.	
457	426	427			90	7	60(PHE)	4.5	
458	427	428			89	10	36(SER)	17.	
459	428	429			91	6	26(MET)	35.	
460	429	430			92	10	31(HIS)	3.1	
461	430	431			93	10	59(GLU)		
462	431	432			94	8	52(ALA)	13.	
463	432	433			94	7	82(LEU)	5.9	
464	433	434			95	7	43(ASP)	15.	
465	434	435			95	10	45(ASN)	21.	
466	435	436			95	12	38(HIS)	30.	
467	437	437			94	10	26(ASP)	36.	
468	437				63	6	35(SER)	7.6	
469	438	438			94	7	90(VAL)	2.	
470	439	439			94	7	43(GLN)	15.	
471	440	440			90	6	64(LYS)	8.4	
472	441	441			95	7	53(SER)	13.	
473	442	442			94	9	52(GLN)	16.	
474	443	443			95	1	1(ILS)		
475	444	444			95	7	64(SER)	12.	
476	445	445			95	7	39(ARG)	17.	
477	446	446			95	8	42(SER)	18.	
478					95	10	44(ASP)	22.	
					66	4	59(GLY)	3.4	
					43	4	36(LYS)	4.8	